Impact of Temporal Structure on SIR Epidemic Spread in Activity-Driven Networks: A Comparative Study with Static Aggregated Networks

Abstract—The role of temporal network structure in epidemic spreading remains a central challenge in computational epidemiology. This paper investigates how an infectious disease, modeled via the Susceptible-Infectious-Removed (SIR) framework with a basic reproduction number $R_0 = 3$, propagates through an activity-driven temporal network of 1000 nodes—where each node activates with probability $\alpha = 0.1$ and forms $m = 2$ instantaneous contacts—in comparison to its time-aggregated static counterpart in which edge weights represent contact frequencies. Through simulation and quantitative analysis, we find that the temporal ordering and sparsity of interactions in the activity-driven scenario significantly diminish outbreak severity and peak infection compared to the static network, even under identical R_0, highlighting the critical importance of temporal effects for epidemic prediction and control.

I. INTRODUCTION

The spread of infectious diseases depends sensitively on the structure of contact networks over which transmission occurs [1], [2], [3]. Traditional epidemic models, such as the SIR framework, are often analyzed on static graphs that aggregate all contacts over a period, ignoring the order and timing of interactions. However, real-world contact patterns are dynamic, with temporally fluctuating activity and intermittent ties that may strongly alter outbreak trajectories [4], [5], [6].

A canonical paradigm for temporal networks is the activity-driven model [4], in which each of N nodes is assigned an intrinsic activity rate, and at each time step, active nodes form a small number m of transient edges. In this system, the instantaneous network is sparse and rapidly changing, potentially limiting the ability of pathogens to traverse the network compared to a weighted static representation where all links (regardless of when they occurred) are always active.

Recent studies have argued that aggregation of contacts can lead to a dramatic overestimation of epidemic size and speed; specifically, the temporal structure can create bottlenecks that restrict the flow of infection, even for the same average number of contacts and a fixed R_0 [7], [8]. Yet, the quantitative impact of these effects for SIR epidemics on activity-driven versus static networks, for identical population and R_0, remains an open and practically relevant question.

In this work, we address this question through a computational experiment. We simulate SIR dynamics (with $R_0 = 3$) in both an activity-driven temporal network and its aggregated static counterpart, where connections are weighted by frequency of past interactions, for $N = 1000$, $\alpha = 0.1$, $m = 2$. By analyzing epidemic curves, peak infection, outbreak du-

ration, and final epidemic size, we elucidate the substantial influence of temporal network features—specifically, the ordering and concurrency of contacts—on disease spread. Our results highlight the potential pitfalls of using static network representations for infectious disease forecasting in dynamic populations.

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